

Table S1. ClustalW multiple sequence alignment for parent CBH II enzyme catalytic domains. Blocks 2, 4, 6 and 8 are denoted by boxes and grey shading. Blocks 1, 3, 5 and 7 are not shaded.

H.inso	GNPFEGVQLWANNYYRSEVHTLAIPQITDPALRAAASAVAEVPSFQWLDRNVTVDTLVQ	60
C.ther	GNPFSGVQLWANTYYSSSEVHTLAIPSLP-PELAAKAAKVAEVPSFQWLDRNVTVDTLFSG	59
H.jeco	GNPFVGVTPWANAYYASEVSSLAIPSLT-GAMATAAAAVAKVPSFMWLDL-LDKTFLMEQ	58
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H.inso	TLSEIREANQAGANPQYAAQIVVYDLPDRDCAAAASNGEWAIANNGVNNYKAYINRIREI	120
C.ther	TLAEIRAANQORGANPPYAGIFVVYDLPDRDCAAAASNGEWSIANNGANNYKRYIDRIREL	119
H.jeco	TLADIRTANKNGN--YAGQFVVYDLPDRDCAALASNGEYSIADGGVAKYKNYIDTIRQI	116
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H.inso	LISFSDVRTILVIEPDSLANNMVTNMNPKCSGAASYRELTIYALKQLDLPHVAMYMDAG	180
C.ther	LIQYSDIRTILVIEPDSLANNMVTNMNPKCSNAASYKELTVYALKQLNLPHVAMYMDAG	179
H.jeco	VVEYSDIRTLLVIEPDSLANNLVTNLGTPKCANAQSAYLECINYAVTQLNLPNVAMYLDAG	176
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H.inso	HAGWLGWPANIQPAAELFAKIYEDAGKPRAVRGLATNVANYNAWSVSSPPPYTSPNPNYD	240
C.ther	HAGWLGWPANIQPAAELFAQIYRDAGRPAAVRGLATNVANYNAWSIASPPSYTSPNPNYD	239
H.jeco	HAGWLGWPANQDPAAQLFANVYKNASSPRALRGLATNVANYNGWNITSPPSYTQGNVAVYN	236
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H.inso	EKHYIEAFRPLLEARGFE-AQFIVDQGRSGKQPTGQKEWGHWCNAIGTGFGMRPTANTGH	299
C.ther	EKHYIEAFAPLLRNQGF-AKFIVDTGRNGKQPTGQLEWGHWCNVKGTGFGVRPTANTGH	298
H.jeco	EKLYIHAIGPLLANHGWSNAFFITDQGRSGKQPTGQQQWGDWCNVIGTGFGIRPSANTGD	296
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H.inso	QYVDAFVWVKPGGEC DGTSDTTAARYDYHCGLEDALKPAPEAGQWFNEYFIQLLRNANPF	359
C.ther	ELVDAFVWVKPGGES DGTSDTSAARYDYHCGLSDALTPAPEAGQWFQAYFEQLLINANPF	358
H.jeco	SLLDSFVWVKPGGEC DGTSDSSAPRFD SHCALPDALQAPQAGAWFQAYFVQLLTNANPS	356
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H.inso	F- 360	
C.ther	F- 359	
H.jeco	FL 358	
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